

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/601,311A  
Source: 1Fw16  
Date Processed by STIC: 7/19/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 07/19/2006

PATENT APPLICATION: US/10/601,311A

TIME: 09:07:20

Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt

Output Set: N:\CRF4\07192006\J601311A.raw

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3 <110> APPLICANT: Takeda San Diego, Inc.
5 <120> TITLE OF INVENTION: CRYSTALLIZATION OF AKT3
7 <130> FILE REFERENCE: AKT3-5001-C1
9 <140> CURRENT APPLICATION NUMBER: 10/601,311A
10 <141> CURRENT FILING DATE: 2003-06-20
12 <150> PRIOR APPLICATION NUMBER: 60/400,207
13 <151> PRIOR FILING DATE: 2002-07-31
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 479
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: MISC_FEATURE
27 <222> LOCATION: (1)..(479)
28 <223> OTHER INFORMATION: Amino acid sequence for full length human wild type AKT3
30 <300> PUBLICATION INFORMATION:
31 <308> DATABASE ACCESSION NO: Genbank/NP_005456
32 <309> DATABASE ENTRY DATE: 2002-04-04
33 <313> RELEVANT RESIDUES: (1)..(461)
35 <400> SEQUENCE: 1
37 Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly
38 1 5 10 15
41 Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
42 20 25 30
45 Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
46 35 40 45
49 Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
50 50 55 60
53 Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
54 65 70 75 80
57 Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
58 85 90 95
61 Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
62 100 105 110
65 Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
66 115 120 125
69 Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
70 130 135 140
73 Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
74 145 150 155 160
77 Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met

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78          165          170          175
81 Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
82          180          185          190
85 Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
86          195          200          205
89 Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
90          210          215          220
93 Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
94 225          230          235          240
97 Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
98          245          250          255
101 Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
102          260          265          270
105 Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
106          275          280          285
109 Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
110          290          295          300
113 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
114 305          310          315          320
117 Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met
118          325          330          335
121 Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
122          340          345          350
125 Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
126          355          360          365
129 Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
130          370          375          380
133 Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
134 385          390          395          400
137 Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
138          405          410          415
141 Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
142          420          425          430
145 Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
146          435          440          445
149 Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
150          450          455          460
153 Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu
154 465          470          475
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 978
159 <212> TYPE: DNA
160 <213> ORGANISM: Homo sapiens
163 <220> FEATURE:
164 <221> NAME/KEY: misc_feature
165 <222> LOCATION: (1)..(978)
166 <223> OTHER INFORMATION: Human cDNA sequence encoding residues 136-461 of AKT3
168 <400> SEQUENCE: 2
169 tctacaacc atcataaaag aaagacaatg aatgattttg actatttgaa actactaggt      60

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171 aaaggcactt ttgggaaagt ttttttggtt cgagagaagg caagtggaaa atactatgct      120
173 atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact      180
175 gaaagcagag tattaaagaa cactagacat ccctttttta catccttgaa atattccttc      240
177 cagacaaaag accgtttgtg ttttgtgatg gaatatgtta atggggggcga gctgtttttc      300
179 cttttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt      360
181 gtctctgcct tggactatct acattccgga aagatttgtt accgtgatct caagttggag      420
183 aatctaatagc tggacaaaga tggccacata aaaattacag attttggact ttgcaaagaa      480
185 gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca      540
187 gaggtgttag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgtc      600
189 atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaacttttt      660
191 gaattaatat taatggaaga cattaaattt cctcgaacac tctcttcaga tgcaaaatca      720
193 ttgctttcag ggctcttgat aaaggatcca aataaacgcc ttggtggagg accagatgat      780
195 gcaaaagaaa ttatgagaca cagtttcttc tctggagtaa actggcaaga tgtatatgat      840
197 aaaaagcttg tacctccttt taaacctcaa gtaacatctg agacagatac tagatatatt      900
199 gatgaagaat ttacagctca gactattaca ataacaccac ctgaaaaata tgatgaggat      960
201 ggtatggact gcatggac
204 <210> SEQ ID NO: 3
205 <211> LENGTH: 556
206 <212> TYPE: PRT
207 <213> ORGANISM: Artificial
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Amino acid sequence for residues 136-461 of AKT3 with a

```

cleavable

```

211      intein tag and cleavage site
214 <220> FEATURE:
215 <221> NAME/KEY: MISC_FEATURE
216 <222> LOCATION: (1)..(226)
217 <223> OTHER INFORMATION: Cleavable N-terminal intein tag
219 <220> FEATURE:
220 <221> NAME/KEY: MISC_FEATURE
221 <222> LOCATION: (227)..(230)
222 <223> OTHER INFORMATION: CRSL cleavage site
224 <220> FEATURE:
225 <221> NAME/KEY: MISC_FEATURE
226 <222> LOCATION: (231)..(556)
227 <223> OTHER INFORMATION: Amino acid sequence for resisues 136-461 of AKT3
229 <400> SEQUENCE: 3
231 Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp
232 1          5          10          15
235 Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly
236          20          25          30
239 Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu
240          35          40          45
243 Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn
244          50          55          60
247 Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile
248 65          70          75          80
251 Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp
252          85          90          95
255 Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu

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256				100				105				110					
259	Glu	Ser	Ala	Lys	Val	Ser	Arg	Val	Phe	Cys	Thr	Gly	Lys	Lys	Leu	Val	
260			115					120				125					
263	Tyr	Ile	Leu	Lys	Thr	Arg	Leu	Gly	Arg	Thr	Ile	Lys	Ala	Thr	Ala	Asn	
264		130					135					140					
267	His	Arg	Phe	Leu	Thr	Ile	Asp	Gly	Trp	Lys	Arg	Leu	Asp	Glu	Leu	Ser	
268	145					150					155					160	
271	Leu	Lys	Glu	His	Ile	Ala	Leu	Pro	Arg	Lys	Leu	Glu	Ser	Ser	Ser	Leu	
272				165						170					175		
275	Gln	Leu	Ser	Pro	Glu	Ile	Glu	Lys	Leu	Ser	Gln	Ser	Asp	Ile	Tyr	Trp	
276			180					185					190				
279	Asp	Ser	Ile	Val	Ser	Ile	Thr	Glu	Thr	Gly	Val	Glu	Glu	Val	Phe	Asp	
280		195						200					205				
283	Leu	Thr	Val	Pro	Gly	Pro	His	Asn	Phe	Val	Ala	Asn	Asp	Ile	Ile	Val	
284		210					215					220					
287	His	Asn	Cys	Arg	Ser	Leu	Ser	Thr	Thr	His	His	Lys	Arg	Lys	Thr	Met	
288	225				230						235					240	
291	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	Lys	
292				245						250					255		
295	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Tyr	Ala	Met	Lys	
296			260					265					270				
299	Ile	Leu	Lys	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	Glu	Val	Ala	His	Thr	
300			275					280					285				
303	Leu	Thr	Glu	Ser	Arg	Val	Leu	Lys	Asn	Thr	Arg	His	Pro	Phe	Leu	Thr	
304		290					295					300					
307	Ser	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	Lys	Asp	Arg	Leu	Cys	Phe	Val	Met	
308	305				310					315						320	
311	Glu	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	Arg	
312				325						330					335		
315	Val	Phe	Ser	Glu	Asp	Arg	Thr	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	Ser	
316			340					345					350				
319	Ala	Leu	Asp	Tyr	Leu	His	Ser	Gly	Lys	Ile	Val	Tyr	Arg	Asp	Leu	Lys	
320			355					360				365					
323	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	Asp	
324		370					375					380					
327	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Thr	Asp	Ala	Ala	Thr	Met	Lys	Thr	
328	385				390					395						400	
331	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	Asn	
332				405						410					415		
335	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	Tyr	
336			420					425					430				
339	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	Lys	
340			435					440					445				
343	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Asp	Ile	Lys	Phe	Pro	Arg	Thr	Leu	
344		450					455					460					
347	Ser	Ser	Asp	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Ile	Lys	Asp	Pro	
348	465				470					475						480	
351	Asn	Lys	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	Glu	Ile	Met	Arg	
352				485						490					495		

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355 His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys  
 356 500 505 510  
 359 Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg  
 360 515 520 525  
 363 Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro  
 364 530 535 540  
 367 Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
 368 545 550 555  
 371 <210> SEQ ID NO: 4  
 372 <211> LENGTH: 330  
 373 <212> TYPE: PRT  
 374 <213> ORGANISM: Artificial  
 376 <220> FEATURE:  
 377 <223> OTHER INFORMATION: CRSL fused to the N-terminal of amino acid residues 136-461  
 of  
 378 AKT3  
 381 <220> FEATURE:  
 382 <221> NAME/KEY: MISC\_FEATURE  
 383 <222> LOCATION: (1)..(4)  
 384 <223> OTHER INFORMATION: CRSL cleavage site  
 386 <220> FEATURE:  
 387 <221> NAME/KEY: MISC\_FEATURE  
 388 <222> LOCATION: (5)..(330)  
 389 <223> OTHER INFORMATION: Amino acid sequence for residues 136-461 of AKT3  
 391 <400> SEQUENCE: 4  
 393 Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met Asn Asp  
 394 1 5 10 15  
 397 Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile  
 398 20 25 30  
 401 Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys Ile Leu  
 402 35 40 45  
 405 Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Leu Thr  
 406 50 55 60  
 409 Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr Ser Leu  
 410 65 70 75 80  
 413 Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met Glu Tyr  
 414 85 90 95  
 417 Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe  
 418 100 105 110  
 421 Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu  
 422 115 120 125  
 425 Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys Leu Glu  
 426 130 135 140  
 429 Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly  
 430 145 150 155 160  
 433 Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr Phe Cys  
 434 165 170 175  
 437 Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr  
 438 180 185 190  
 441 Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/19/2006  
PATENT APPLICATION:    US/10/601,311A      TIME: 09:07:21

Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt  
Output Set: N:\CRF4\07192006\J601311A.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4

**VERIFICATION SUMMARY**

DATE: 07/19/2006

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TIME: 09:07:21

Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt

Output Set: N:\CRF4\07192006\J601311A.raw